

## AMENDMENTS TO THE CLAIMS

1. (Currently amended) A system for ~~designing a~~ determining a location of a target sequence in a genome sequence ~~probes using heterogeneous genetic information~~, comprising:

a storage unit storing a crosslink map, wherein the crosslink map comprises a record for a sequence information for each version of a genome sequence comprising the sequence information ~~having records according to the version of a genome sequence~~;

an information search unit, for searching for the identifier information and sequence information corresponding to a target genetic information sequence among the ~~genetic information about the genome sequence records~~ in the crosslink map; and

a location estimation unit, for determining a reference group made up of comprising reference genetic sequence information for an organism, wherein the reference sequence information is represented in the crosslink map by ~~which is contained in more than a predetermined number in an organism of records~~, calculating a difference values of the a start positions and the an end positions of the a reference genetic sequence information based on obtained from the crosslink map, and determining the a location of the target genetic information sequence on in the latest a genome sequence by a location shift corresponding to the difference values.

2. (Currently amended) The system of claim 1, further comprising  
an information integration unit, for receiving genome sequence data corresponding to entries recorded on the crosslink map from various sources about the genome sequence and transforming the received data into data formats recognized by the crosslink map.

3. (Currently amended) The system of claim 1, wherein ~~entries recorded a~~ a record for a sequence information ~~in on~~ the crosslink map comprises

a name of the a genome sequence,  
a version of the genome sequence,  
an identifier of a genetic sequence information ~~about in~~ the genome sequence,  
a start position and an end position of the genetic sequence information ~~on in~~ the genome sequence, and  
a length of the genetic sequence information ~~about in~~ the genome sequence.

4. (Currently amended) The system of claim 1, wherein the location estimation unit determines the location of the target genetic information sequence by assigning a higher priority to the calculated difference values calculated with respect to genetic for a reference sequence information which is contained in a more number in an organism represented in the crosslink map by a larger number of records.

5. (Currently amended) The system of claim 1, wherein the location estimation unit comprises:

an estimation region setting portion for calculating a difference values of the a start positions and the an end positions of genetic sequence information in the crosslink map excluded from the reference group based on the crosslink map and setting an estimation region for the location of the target genetic information sequence on in the latest genome sequence based on the calculated difference values; and

a location determining portion for determining the location of the target genetic information sequence in the estimation region of the latest genome sequence by a location shift corresponding to the calculated difference values calculated with respect to for the reference genetic sequence information.

6. (Currently amended) The system of claim 1, wherein the location estimation unit further comprises

an updating portion for updating the reference group in such a way to, calculate calculating a difference values of the a start positions and the an end positions of for each sequence genetic information which is commonly present on individual versions of the genome sequence in the updated reference group, and selecting genetic sequence information in which the calculated difference values are is within a predetermined range.

7. (Currently amended) A method of ~~designing a~~ determining a location of a target ~~probes~~  
~~sequence using in a genome sequence~~ heterogeneous genetic information, the method comprising:  
inputting a target sequence;  
~~creating a crosslink map having records according to the version of a genome sequence;~~  
~~searching for the identifier~~ information and sequence information corresponding to the target  
~~genetic information~~ sequence ~~among the genetic information about the genome sequence in the a~~  
~~crosslink map,~~  
wherein the crosslink map comprises a record for a sequence information for each version of a  
genome sequence comprising the sequence information;  
~~determining a reference group made up of~~ comprising reference genetic sequence information,  
wherein the reference sequence information for an organism which is contained represented in the  
crosslink map in by more than a predetermined number in an organism of records;  
~~calculating a difference values of the a start positions and the an end positions of the a reference~~  
~~genetic sequence~~ information based on obtained from the crosslink map; and  
~~determining the a location of the target genetic information~~ sequence on in the latest a genome  
~~sequence by a location shift corresponding to the difference values.~~

8. (Currently amended) The method of claim 7, wherein ~~entries a record for a sequence~~  
~~information recorded on in~~ the crosslink map comprises  
a name of ~~the a~~ genome sequence,  
a version of the genome sequence,  
an identifier ~~offor the a~~ genetic sequence information about in the genome sequence,  
a start position and an end position of the ~~genetic sequence~~ information on in the genome  
sequence, and  
a length of the ~~genetic sequence~~ information about in the genome sequence.

9. (Currently amended) The method of claim 7, wherein determining the location of the  
target ~~genetic information~~ sequence is carried out by  
assigning a higher priority to the difference values calculated ~~with respect to for genetic a~~  
~~reference sequence~~ information which is represented contained in a more number in an organism in the  
crosslink map by a larger number of records.

10. (Currently amended) The method of claim 7, further comprising updating the reference group; ~~in such a way to calculate~~ calculating a difference values of the a start positions and the an end positions of for each genetic sequence information in the updated reference group; which is commonly present on individual versions of the genome sequence and selecting genetic sequence information in which the calculated difference values are ~~is~~ within a predetermined range.

11. (Currently amended) The method of claim 7, wherein determining the location of the target genetic information comprises:  
 calculating a difference values of the a start positions and the an end positions of a genetic sequence information obtained from the crosslink map, wherein the sequence information was excluded from the reference group; based on the crosslink map and  
 setting an estimation region for the location of the target ~~genetic information~~ sequence on the latest genome sequence based on the calculated difference values; and  
 determining the location of the target ~~genetic information~~ sequence in the estimation region of the latest genome sequence by a location shift corresponding to the calculated difference values ~~calculated with respect to for~~ the reference ~~genetic sequence~~ information.

12. (Currently amended) A computer readable medium having embodied thereon a computer program for ~~a the~~ method of determining a location of a target sequence in a genome sequence of claim 7,  
~~wherein the computer readable medium is not a carrier wave. designing a probes using heterogeneous genetic information, the method comprising:~~  
~~creating a crosslink map having records according to the version of a genome sequence;~~  
~~searching for the identifier and sequence information corresponding to target genetic information among the genetic information about the genome sequence in the crosslink map;~~  
~~determining a reference group made up of reference genetic information which is contained in more than a predetermined number in an organism;~~  
~~calculating difference values of the start positions and the end positions of the reference genetic information based on the crosslink map; and~~  
~~determining the location of the target genetic information on the latest genome sequence by a location shift corresponding to the difference values.~~

13. (New) The method of claim 8, wherein the location of the target sequence is determined in the version of the genome sequence represented in the crosslink map which is the most recent version of the genome sequence.

14. (New) The method of claim 7, further comprising displaying the location of the target sequence in the genome sequence.